Figure 1



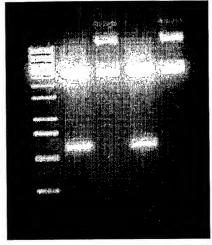
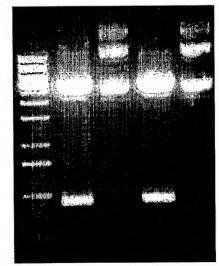


Figure 2



#### 2/11

#### Figure 3A

### Figure 3B

#### 3 / 11

### Figure 3C

### Figure 3D

### 4/11

# Figure 3E

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Query:	82	AAELAGVLEATAAAKTAVEQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 141
		AAELA LE+T AAK + EQ+RE TRA L K S EQ
Sbjct:	793	AAELASQLESTTAAKMSAEQDRESTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQD 852
Query:	142	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
		+ST A K + EQDRE+TRAT
Sbjct:	853	RESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQDRESTRAT 898

# Figure 3F

Query:	29	EQEREKTRTALEGRAAELARKLEATASAKNLVEQDXXXXXXXXXXXXXIAEVR 81
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Ouerv:	82	AAELAGVLEATAAAKTAVEQERERTRAALXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
20027		AAELA LE+T AAK + EQ+RE TRA L K S EQ
Sbjct:	832	AAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTAAKMSAEQD 891
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Query:	142	++TAA KS+ EQDRENTRA
Sbjct:	892	RESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRA 936

### 5/11

## Figure 4

LCIMM KEIMM	121 1	GAGCAGCATCGCGAATCCGAGGCGCGCGCGCGCGGAGCCAGCTGGAGGCC	180 1
DDIMM	1	${\tt GAGCAGCTTCGTGAATCCGAGGCGCGCGCGCGGAGCTGAAAGCCGAGCTGGAGGCC}$	60
LCIMM	181	ACTGCTGCTGCGAAGATGTCAGCGGAGCAGGACCGCGAGAACACGAGGGCCACGCTAGAG	240 3
KEIMM DDIMM	1 61	ACTGCTGCGAAGACGTCGGTGGAGCAGGAGCGTGAGAAGACGAG	107
LCIMM KEIMM	241 4	CAGCAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGGCGAGCTGGAGTCCACT CAGCAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAAGCTGATGCGGAAGTTAGAGGCGACT	300 63
DDIMM	108	CA-CCGCTCTCGAGGGCCCCCTGCGGAGCTCGCTAAACTGGAGGCGACT	159
LCIMM KEIMM	301 64 160	ACTCCTGCGAAGATGTCACCCGAGACCAGGACCACGAGAGCACGAGAGCAGCAGGCTAGAGCAGGCTAGAGCAGGCTGCTGCGAAGTCGTCGCGCGAGACCACGAGACCACGAGACCACGAGACCACGTTCGAGCAGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGACCAGGACCACGACCACC	360 123 219
DDIMM		CAGCTTCGTGACTCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACTACT	420
KEIMM DDIMM	361 124 220	CAGCTTCGTGACTCCGAGGAGCGCGCGCGGGGGCTGGCGAGCCAGCTGGAGTCCACTGCT CAGCTTCGCGAATCCGAGGAGCACGCTGCGGAGCTGAAGGCCCAGCTGGAGTCCACTGCT CGACTTCGTATTGCTGAGGTGCGCGCGCGGAGCTGCGAGGAGTGCTGGAGGCCACTGCT	183 279
LCIMM KEIMM	421 184	GCTGCGAAGATGTC <mark>A</mark> GCGGAGCAGGACCGGGAGAGCACGACGCCACGCTAGAGCAGCAG GCTGCGAAGACGTC <mark>G</mark> GCGGAGCAGGACCGGGAGAACACGAGGGCCGCGTTGGAGCAGCGG	480 243
DDIMM	280	GCTGCGAAGA <mark>C</mark> GGCGGTGGAGCAGGAGCGCGGCGCCTTGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	339
LCIMM KEIMM	481 244	CTTCGCGAATCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGTCCACTACTGCT CTTCGCGAATCCGAGGAGCGCGCTGCGGAGCTGGCGAGCCAGCTGGAGCCCACTGCTGCT	540 303 399
DDIMM	340	CTCCGCGAATCCGAGGCGCGCGCTGCGGAGCTGGCTGCGCAGCTGGAAGCCGCTGCTGCCG	
LCIMM KEIMM DDIMM	541 304 400	GCGAAG <mark>ATGTCAGC</mark> GGAGCAGGACCGCGAGAGCACGCCACGCTAGAGC <mark>AGCAGC</mark> TT GCGAAG <mark>TC</mark> GTCGGCGGAGCAGGACCGCGAGAACACGAGGGCCACGCTAGAGCAGCAGCTT GCGAAG <mark>AC</mark> GTCGGTGGAGCAGGAGCGTGAGAACACGAGGGCCACCTTGGAGGAGCGGTTG	600 363 459
LCIMM	601		660 423
KEIMM DDIMM	364 460	CGCGAATCCGAGGCGCGCTGCGGAGCTGGCAGGCGCGCTAAAGAGCACTGCTGCTGTT	519
LCIMM KEIMM DDIMM	661 424 520	AAGTC <mark>GT</mark> CG <mark>GC</mark> GGAGCAGGACCGCGAGAACACGAGGGCCA	720 465 561

### 6/11

## Figure 5

LCIMM	1	Leqqlreseeraaelasqleataaakssaeqdrentratleqqlresearaaelasqlea	60
KEIMM	1.	-EQQLRDSEERAAELMRKLEATAAAKSSAEQDRENTRATLEQQLRESEEHAAELKAQLES	59
DDIMM	1	-eqqlresearaaelkaeleataaaktsveqerektrtalegraaelarklea	52
LCIMM	61	taäakmsaeodrentratleoolrdseeraaelasolesttaakmsaeodrestratleo	120
KEIMM	60	ta <mark>a</mark> ak <mark>tsaeqdren</mark> tra <mark>aleor</mark> lreseeraaelasole <mark>a</mark> taaakssaeodrentrauleo	119
DDIMM	53	TASAKNLVEQDRERTRATLEERLRIAEVRAAELAGVLEATAAAKTAVEQERERTRAALEQ	112
LCIMM	121	QLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQQLRESEERAAELASQLESTTA	
KEIMM	120	Surian por transposition and sure of the s	155
DDIMM	113	QLRESE <mark>ARAAELAÄQLEÄAAAAK</mark> TSVEQERENTRATLEERLRLAEVRAAELAARLKSTAA	172
LCIMM	181	${\tt AKMSAEQDRESTRATLEQQLRDSEERAAELASQLEATAAAKSSAEQDRENTRAALEQQLR}$	240
KEIMM	155		155
DDIMM	173	VKSAMEQDRENTRAT	187
		Figure 6	
LCIMM	. 1	LEQQLRESEERAAELASQLEATAAAKSSAEQDRENTRATL <mark>EQQLRESEARAAEL</mark> ASQ <mark>LEA</mark>	60
DDIMM	1	EQQLRESEARAAELKAELEA	20
LCIMM	61	TAAAKMSAEQDRENTRATLEQQLRDSEERAAELASQLESTTAAKMSAEQDRESTRATLEQ	120
DDIMM	21	TAAAKTSVEQEREKTRTALEGRAAELARKLEATASAKNLVEQDRERTRATLEE	73
LCIMM	121	<u>Ö</u> lr <mark>dseb</mark> raaela <mark>so</mark> lesttaak <mark>msaeod</mark> restratleoolrese <mark>b</mark> raaela <mark>s</mark> olestta	
DDIMM	74	RLRIAEVRAAELAGVLEATAAAKTAVEQERERTRAALEQQLRESEARAAELAAQLEAAAA	133
LCIMM	181		
DDIMM	134	AKTSVEQERENTRATLEERLRLAEVRAAELAARLKSTAAVKSAMEQDRENTRAT	187

Figure 7

KEIMM	1	EQQLRDSEERAAELMRKLEATAAAKSSAEQ	30
DDIMM	1	EQQLRESEARAAELKAELEATAAAKTSVEQEREKTRTALEGRAAELARKLEATASAKNLV	60
KEIMM	30	DRENTRATLEOOLRESEEHAAELKAQLESTAAAKTSAEODRENTRAALEORLRESEER	88
DDIMM	61	eqdre <mark>rtratleer</mark> lr <mark>iaevraaelagvlea</mark> taaaktaveqerertraaleqqlresear	120
KEIMM	89	aaela <mark>s</mark> qlea <mark>taaakssa</mark> eqdrentratle <mark>qq</mark> lr <mark>esea</mark> raaela <mark>sqle</mark> staa <mark>a</mark> kssaeqd	148
DDIMM	121	AAELAAQLEAAAAAKTSVEQERENTRATLE <mark>ER</mark> LR <mark>LAE</mark> VRAAELA <mark>AR</mark> LKSTAAVKSAMEQD	180
KEIMM	149	RENTRAT 155	
DDIMM	181	RENTRAT 187	

Figure 8

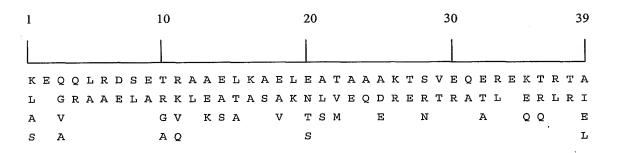


Figure 9

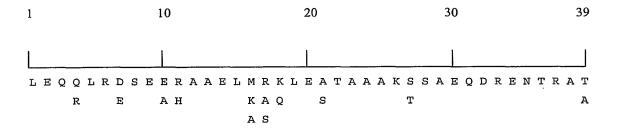


Figure 10

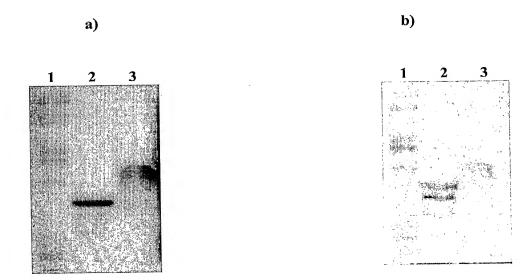
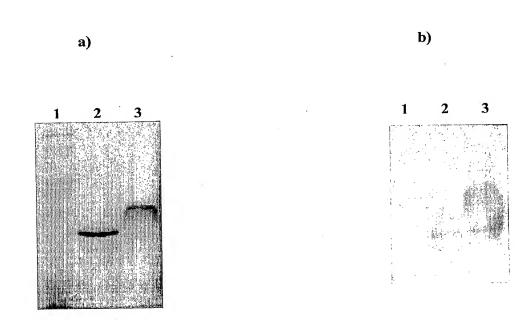


Figure 11



9/11

Figure 12

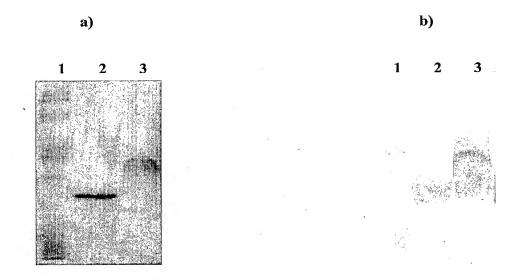


Figure 13

a) b)

Figure 14

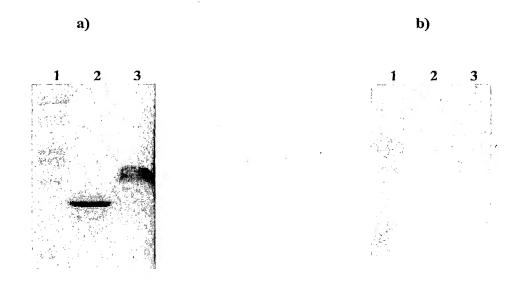
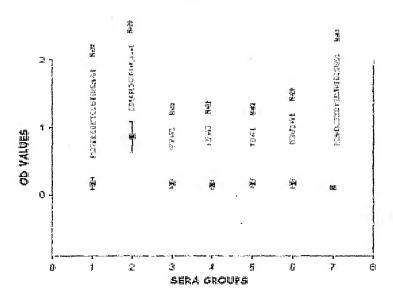
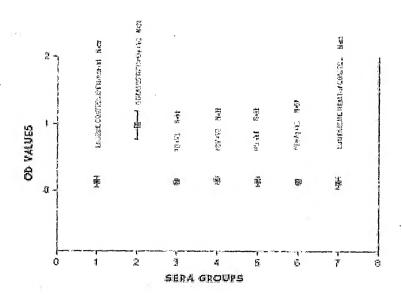


Figure 15



Mean	0.1670	0.8665	0.1634	0.1396	0.1663	0.1636	0.1080
Std.Dev	0.0882	0.2182	0.0598	0.0584	0.0534	0.0615	0.0295

Figure 16



Mean	0.1290)	0.9730)	0.1300)	0.1545)	0.1456)	0.1363)	0.12191
Std.Dev.	0.0716	0.2096	0.0419	0.0548	0.0705	0.0456	0.0796